

Genome version 5.1.3
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EM nucleic nucleic search, using sw model

Run on: April 16, 2003, 22:48:44 : Search time 658 Seconds

(without alignments)
10021.050 Million cell updates/sec

Title: US-09-954-679-3

Perfect score: 2928
Sequence: 1 aatcccaatracatcaaa.....qqqqccttqatqatqat: 2928

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 2274872

Minimum DB seq length: 0

Maximum DB seq length: 60

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: 1: /SUS2/qqdata/a/geneseq/geneseq-emb1/NA1980.DAT: *
2: /SUS2/qqdata/a/geneseq/geneseq-emb1/NA1981.DAT: *
3: /SUS2/qqdata/a/geneseq/geneseq-emb1/NA1982.DAT: *
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6: /SUS2/qqdata/a/geneseq/geneseq-emb1/NA1985.DAT: *
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21: /SUS2/qqdata/a/geneseq/geneseq-emb1/NA2000.DAT: *
22: /SUS2/qqdata/a/geneseq/geneseq-emb1/NA2001A.DAT: *
23: /SUS2/qqdata/a/geneseq/geneseq-emb1/NA2001B.DAT: *
24: /SUS2/qqdata/a/geneseq/geneseq-emb1/NA2002.DAT: *

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	1.2	35	AA146192	Primer for ribonuc
2	45	1.2	45	AA146191	Primer for ribonuc
3	25.6	0.9	60	ABN47026	Human spliced tran
4	25	0.9	48	AAV46756	Nucleotide sequenc
5	25	0.9	48	AAV40768	RNAse L PCR primer
6	24.8	0.8	47	AA266719	Human map-related
7	24.6	0.8	51	AA128761	Human Snp oligonuc
8	24.6	0.8	60	ABN45766	Human spliced tran
9	24.4	0.8	60	ABN47378	Human spliced tran

C 10	23.4	0.8	60	24	ABN40943	Human spliced tran
C 11	23.2	0.8	60	24	ABN48713	Human spliced tran
C 12	22.8	0.8	60	24	ABN46051	Human spliced tran
C 13	22.8	0.8	60	24	ABN42702	Human spliced tran
C 14	22.6	0.8	40	17	AA128117	Probe for human co
C 15	22.6	0.8	60	24	ABN46589	Human spliced tran
C 16	22.6	0.8	60	24	ABN48697	Human spliced tran
C 17	22.4	0.8	57	16	AA122865	Human gene stimula
C 18	22.4	0.8	58	24	AA155233	Human cation chan
C 19	22.4	0.8	59	21	AA296905	5' overhang gene
C 20	22.2	0.8	51	22	AA128440	Human Snp oligonuc
C 21	22.2	0.8	51	22	AA159488	cDNA encoding more
C 22	22.2	0.8	51	22	AA188455	Human digestive by
C 23	22.2	0.8	60	21	AA257910	Yeast tetacycline
C 24	22.2	0.8	60	24	ABN43058	Human spliced tran
C 25	22.2	0.8	60	24	ABN43058	Human Snp oligonuc
C 26	22.2	0.8	58	19	AAV28969	Human MCM with na
C 27	22.2	0.8	60	24	ABN48594	Human spliced tran
C 28	22.2	0.8	60	24	ABN40101	Human spliced tran
C 29	22.2	0.8	60	24	ABN40981	Human spliced tran
C 30	21.8	0.7	39	19	AAV13828	Primer for canine
C 31	21.8	0.7	39	20	AA15623	PCR primer for mo
C 32	21.8	0.7	39	20	AA15623	PCR primer #7 Un
C 33	21.8	0.7	49	22	AA154386	Acetyl repeat mod
C 34	21.8	0.7	48	24	AB151939	Human Snp flankin
C 35	21.8	0.7	51	22	AA138644	Human Snp flankin
C 36	21.8	0.7	51	23	AA100653	Human gene stimula
C 37	21.8	0.7	52	16	AA121611	Staphylococcus au
C 38	21.8	0.7	60	18	AAV75963	Human spliced tran
C 39	21.8	0.7	60	24	ABN49878	Aspergillus foot of
C 40	21.6	0.7	51	16	AAV98582	Aspergillus foot of
C 41	21.6	0.7	51	16	AAV98581	Human Snp oligonuc
C 42	21.6	0.7	51	22	AA130771	Human Snp oligonuc
C 43	21.6	0.7	51	22	AA138424	Human Snp flankin
C 44	21.6	0.7	60	24	ABN42202	Human spliced tran
C 45	21.6	0.7	60	24	ABN47958	Human spliced tran

ALIGNMENTS

RESULT 1

AA146192/c

ID AA146192 standard; DNA: 45 bp.

AC AA146192;

XX AA146192;

XX 22-JUL-1997 (first entry)

DT Primer for ribonuclease L cDNA amplification.

DE Primer for ribonuclease L cDNA amplification.

XX Bovine; 2',5'-oligoadenylate acid synthase; plant

RNA virus; ribonuclease L; cucumber mosaic virus; primer, 1996; 88.

XX Synthetic.

OS Synthetic.

PN W09638044-A1.

XX 05 DEC-1996.

XX 31 MAY-1996; 96WO 0101485.

FF 08-MAR-1996; 96JP 0052010.

PR 31-MAY-1996; 96JP 0133741.

PR 01 NOV-1996; 96JP 0285401.

XX (KIRI) KIRIN BEER KK.

XX Ishida L, Iqawa T, Yoshioka M.

XX WPI; 1997-044004/03.

XX Plants resistant to attack by RNA viruses have

PT

PT 2',5'-oligo:adenylic acid synthetase and ribonuclease L genes of
XX animal origin integrated into the plant chromosomes
PS
XX Example 11; Page 22; 74pp; Japanese.
CC AAT46191-92 are primers used to amplify cDNA encoding bovine
CC ribonuclease L (AAT46188). Plants resistant to attack by RNA viruses can
CC be produced by integrating into the plant chromosomes DNA sequences of
CC animal origin encoding 2',5'-oligoadenylic acid synthetase and
CC ribonuclease L. The process is useful for production of plants resistant
CC to attack by damaging RNA viruses (such as cucumber mosaic virus), and is
CC applicable to a broad spectrum of plant species.
XX Sequence 35 BP; 13 A; 5 C; 7 G; 10 T; 0 other;
SQ

Query Match

Best Local Similarity 1.2%; Score 35; 18 18; Length 35;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1502 TCTATATTAAAGGCTGTTCAGAACTACACTGTGC 1536
DB |||||||||||||||||||||||||||||||||||||||
35 TCTATATTAAAGGCTGTTCAGAACTACACTGTGC 1

RESULT 2

AAT46191
ID AAT46191 standard; DNA; 35 BP.
XX
AC AAT46191;
XX
XX
DT 22-JUL-1997 (first entry)
XX
DE Primer for ribonuclease L cDNA amplification.

KW Bovine; 2',5'-oligoadenylic acid synthetase; plant resistance;
KW RNA virus; ribonuclease L; cucumber mosaic virus; primer; PCR; ss.
OS Synthetic.
XX
XX WO9638034-A1.
XX
PD 05-DEC-1996.
XX
PF 31-MAY-1996; 96WO-JP01485.
XX
PR 08-MAR-1996; 96JP-0052010.
PR 31-MAY-1995; 95JP-0133741.
XX
XX 01-NOV-1995; 95JP-0285401.
PA (KIRI) KIRIN BEER KK.
XX
PI Ishida I, Ogawa T, Yoshioka M;
XX
DR WPI; 1997-034004/03.

PT Plants resistant to attack by RNA viruses - have
PT 2',5'-oligo:adenylic acid synthetase and ribonuclease L genes of
PT animal origin integrated into the plant chromosomes
PS
XX Example 11; Page 22; 74pp; Japanese.
CC AAT46191-92 are primers used to amplify cDNA encoding bovine
CC ribonuclease L (AAT46188). Plants resistant to attack by RNA viruses can
CC be produced by integrating into the plant chromosomes DNA sequences of
CC animal origin encoding 2',5'-oligoadenylic acid synthetase and
CC ribonuclease L. The process is useful for production of plants resistant
CC to attack by damaging RNA viruses (such as cucumber mosaic virus), and is
CC applicable to a broad spectrum of plant species
XX
SQ Sequence 35 BP; 11 A; 4 C; 12 G; 8 T; 0 other;
Query Match

Best Local Similarity 1.2%; Score 35; DB 18; Length 35;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1244 CTGGGCTTCTATGAGAGCAAGCAAGTACTGTGCA 1278
DB |||||||||||||||||||||||||||||||||||||||
1 CTGGGCTTCTATGAGAGCAAGCAAGTACTGTGCA 35

RESULT 3

ABN47026
ID ABN47026 standard; DNA; 60 BP.
XX
AC ABN47026;
XX
XX 15-MAY-2002 (first entry)
XX
DE Human spliced transcript detection oligonucleotide SEQ ID NO:19774.

KW Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
OS Homo sapiens.
XX
XX WO200210449-A2.
XX
PD 07-FEB-2002.
XX
PF 20-JUL-2001; 2001WO-1801903.
XX
PR 28-JUL-2000; 2000US-221607P.
PR 02-MAY-2001; 2001US-287724P.
XX
XX (COMP-) COMPUGEN INC.
XX
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Paigler S;
XX
DR WPI; 2002-257383/30.

XX New oligonucleotide libraries comprising oligonucleotides which
XX selectively hybridize to mRNAs transcribed from a transcription unit of
XX a genome, useful for detecting tissue-, pathology-, and
XX developmental-specific genes.
PS Example 1; SEQ ID 19774; 47pp; English.

CC The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the
CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises
CC several oligonucleotides, each capable of hybridizing selectively to a
CC set of messenger RNAs transcribed from a given transcription unit of
CC the genome, which encodes one or more messenger RNA splice variants.
CC The oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterizing the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialized mini
CC libraries to detect transcripts of a sub-transcriptome under a
CC particular biological or pathological state, and so allowing the
CC detection of tissue- and pathology-specific genes such as those genes
CC only expressed in specific tissue under a specific pathological
CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome; and to detect RNA
CC from a particular disorder. ABN27253 to ABN59589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.

Sequence 60 BP; 10 A; 16 C; 19 G; 15 T; 0 other;
Query Match

Best Local Similarity 0.9%; Score 25.6; DB 24; Length 60;
Matches 70.8%; Pred. No. 2.7e+03;


```

PR 21-APP-1998; 980US-0082614.
PR 23-NOV-1998; 980US-0109732.
PA (GENSET)
XX
XX Cohen D, Blumenfeld M, Chumakov I;
XX WPI; 2000 013267/01.
XX Novel biallelic markers used to construct a high density disequilibrium
XX map of the human genome
XX
XX Claim 1; Page 458; 2745pp; English.
XX
XX AAZ65654 to AAZ69578 represent human biallelic markers from the present
XX invention, which contain a polymorphic base at position 24 of their
XX nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
XX primers for the biallelic markers. The biallelic markers of the
XX invention have a variety of uses: they can be used for high density
XX mapping of the human genome, and in complex association studies and
XX haplotyping studies which are useful in determining the genetic basis
XX for disease states. Compositions and methods of the invention can also
XX be useful for the identification of the targets for the development of
XX pharmaceutical agents and diagnostic methods, as well as the
XX characterisation of the differential efficacious responses to and side
XX effects from pharmaceutical agents acting on a disease as well as other
XX treatment.
XX N.B. The SEQ ID NOS 2852, 2913, 2974, 3015, 3096, 3157, 3227, 3297
XX and 3367, are not actually given a sequence in the Sequence Listing
XX from the present invention.
XX
XX Sequence 47 BP; 12 A; 9 C; 8 G; 18 T; 0 other.
XX
Query Match 0.8%; Score 24.8; DB 21; Length 41;
Best Local Similarity 72.7%; Pred. No. 4e+03;
Matches 32, Conservative 0; Mismatches 12, Indels 0, Gaps 0;
QY 2664 GATTATCATCCCATTTTAAAGAACTGAGAACTGAGAACTGAGAGTCAGAG 2707
DB 4 GATTATTTCCCTCTTTTCAAAATCAGCAAGCTCAGGTTTAGAG 47
RESULT 7
AAL28761
ID AAL28761 standard; DNA; 51 BP.
XX
XX AAL28761,
AC
XX
XX 24-JAN-2002 (first entry)
DT
XX
XX Human SNP oligonucleotide #1969.
DE
XX
XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.
XX
XX Homo sapiens.
OS
XX
XX W0200147944-A2.
PN
XX
XX 05-JUL-2001.
PD
XX
XX 28-DEC-2000; 2000WO-US35498.
PF
XX
XX 28-DIC-1999; 99US-0173419.
PR
XX
XX 27-DIC-2000, 2000US-0173419.
PR
XX
XX (CURA-) CURAGEN CORP.
PA

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XX Shimkets RA, Leach M;
XX WPI; 2001-465210/50.
XX
XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
XX oncogenes and histones, useful for diagnosing and treating, e.g.
XX cancer, autoimmune diseases and infections
XX
XX Claim 1; Page 1944; 4143pp; English.
XX
XX The present invention relates to oligonucleotides encoding polymorphic
XX variants of proteins related to amylases, amyloid proteins, angiotensin,
XX apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
XX histones, kinases, colony stimulating factors, complement related
XX proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
XX G-protein coupled receptors and thioesterases. The present sequence is
XX one such oligonucleotide. The oligonucleotides and the peptides encoded
XX by them may be used in the prevention, diagnosis and treatment of
XX diseases associated with inappropriate expression of the proteins listed
XX above. Disorders that may be prevented, diagnosed and/or treated include
XX multifactorial diseases with a genetic component, such as autoimmune
XX diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
XX systemic lupus erythematosus and Grave's disease), inflammation, cancer
XX (e.g. cancers of the bladder, brain, breast, colon and kidney,
XX leukaemia), diseases of the nervous system and an infection of pathogenic
XX organisms.
XX
XX Sequence 51 BP; 22 A; 8 C; 9 G; 12 T; 0 other;
XX
Query Match 0.8%; Score 24.6; DB 22; Length 51;
Best Local Similarity 70.2%; Pred. No. 4.8e+03;
Matches 33, Conservative 0; Mismatches 14, Indels 0, Gaps 0;
QY 2706 ATTTGGCAGAACACATTTGAGAGAAAGCATAAAGCATCAAAATTA 2152
DB 5 ATTTGGAGGAAAAAAGACATGATTCAGCAAAAGATGAATTA 51
RESULT 8
ABN35766
ID ABN35766 standard; DNA; 60 BP.
XX
XX ABN35766,
AC
XX
XX 15-JUL-2002 (first entry)
DT
XX
XX Human spliced transcript detection oligonucleotide SEQ ID NO:8514.
DE
XX
XX Human, mouse, rat, splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX
XX Homo sapiens.
OS
XX
XX W0200210449-A2.
PN
XX
XX 07-FEB-2002.
PD
XX
XX 20-JUL-2001; 2001WO-IP01903.
PF
XX
XX 28-JUL-2000; 2000US-221607P.
PR
XX
XX 02-MAY-2001; 2001US-287724P.
PR
XX
XX (COMP-) COMPUGEN INC.
PA
XX
XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX WPI; 2002-257383/30.
XX
XX New oligonucleotide libraries comprising oligonucleotides which
XX selectively hybridize to mRNAs transcribed from a transcription unit of
XX a genome, useful for detecting tissue-, pathology-, and
XX developmental-specific genes.
XX

```


GenCore version 5.1.3
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SW module: nucleic search, using SW model

Run on: April 16, 2003, 22:40:29 : Search time 8422 Seconds
(without alignments)
10117.907 Million cell updates/sec

Title: US 09 954 679-3
Perfect score: 2928
Sequence: 1 aatcccaattacactcaaa.....gggcactggatgcattgaatt 2928

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2064640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 897812

Minimum DB seq length: 0
Maximum DB seq length: 60

Post processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: GenBank

- 1: qb.ba:*
- 2: qb.bir:*
- 3: qb.in:*
- 4: qb.cm:*
- 5: qb.ov:*
- 6: qb.pat:*
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- 8: qb.pl:*
- 9: qb.pr:*
- 10: qb.ro:*
- 11: qb.sts:*
- 12: qb.sy:*
- 13: qb.un:*
- 14: qb.vi:*
- 15: em.ba:*
- 16: em.fun:*
- 17: em.hum:*
- 18: em.in:*
- 19: em.mn:*
- 20: em.cm:*
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- 22: em.ov:*
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- 24: em.ph:*
- 25: em.pl:*
- 26: em.ro:*
- 27: em.sts:*
- 28: em.un:*
- 29: em.vi:*
- 30: em.bsq.hum:*
- 31: em.bsq.in:*
- 32: em.bsq.of.bet:*
- 33: em.bsq.mus:*
- 34: em.bsq.pln:*
- 35: em.bsq.ro:*
- 36: em.bsq.mam:*
- 37: em.bsq.vrt:*
- 38: em.sy:*
- 39: em.bsq.hum:*
- 40: em.bsq.mus:*
- 41: em.bsq.other:*

Prod. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	0.9	48	6	AR016283
2	24	0.8	54	6	AR064408
3	22.6	0.8	47	6	A21609
4	22.4	0.8	58	6	AX481765
5	22.4	0.8	59	6	AX011418
6	22.4	0.8	60	6	AR201911
7	22.2	0.8	50	9	HSEDA05
8	22.2	0.8	60	6	AR170294
9	22.2	0.8	60	6	AX007121
10	22.2	0.8	60	6	E51067
11	22	0.8	54	19	AF224157
12	21.8	0.7	49	6	AR151069
13	21.8	0.7	49	6	E15325
14	21.8	0.7	51	6	AX116417
15	21.8	0.7	51	6	AX165449
16	21.6	0.7	51	6	A45564
17	21.6	0.7	51	6	A45565
18	21.6	0.7	51	6	AR019428
19	21.6	0.7	51	6	AR019429
20	21.6	0.7	51	6	AX116097
21	21.4	0.7	51	6	AX161191
22	21.4	0.7	51	10	AF428711
23	21.4	0.7	54	9	S60665
24	21.4	0.7	60	6	AX481481
25	21.2	0.7	51	6	AX118094
26	21.2	0.7	51	6	AX190126
27	21.2	0.7	51	6	AX204485
28	21	0.7	57	3	AF049618
29	21	0.7	60	6	AR051681
30	20.8	0.7	50	9	AF057518
31	20.8	0.7	51	6	AX158446
32	20.8	0.7	51	9	AF070628
33	20.8	0.7	54	9	AF078972
34	20.8	0.7	59	6	AX253482
35	20.8	0.7	59	6	AX554804
36	20.8	0.7	60	6	AR160248
37	20.6	0.7	45	6	A05547
38	20.6	0.7	45	6	AR001640
39	20.6	0.7	45	6	AX448220
40	20.6	0.7	45	6	109087
41	20.6	0.7	51	6	AX158947
42	20.6	0.7	54	6	A66662
43	20.6	0.7	54	6	A66663
44	20.6	0.7	57	6	AX257322
45	20.4	0.7	47	6	AX458041

ALIGNMENTS

RESULT 1	AR016283	48 bp	DNA	Linear	Pat. No. 5776690
LOCUS	AR016283	Sequence 6 from patent US 5776690.			
DEFINITION	AR016283				
ACCESSION	AR016283.1	GI:5972560			
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					

Unclassified.
1 (bases 1 to 48)
Vojdani, A. and Mordochai, E.
Detection of chronic fatigue syndrome by decreased levels of RNAse
inhibitor mRNA
Patent: US 5776690-A 6 07 JUN 1998

FEATURES
source
Location/Qualifiers
1..48
/organism="unknown"
BASE COUNT 14 a 11 c 12 g 11 t
ORIGIN

Query Match 0.9%; Score 25; DB 6; Length 48;
Best Local Similarity 100.0%; Pred. No. 2 5e+05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 638 GGACAGTAGAGTCTTCAGCAATTC 662
|||||
DB 1 GGACAGTAGAGTCTTCAGCAATTC 25

RESULT 2
LOCUS AR064498 54 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 71 from patent US 5847096.
ACCESSION AR064498
VERSION AR064498 1 GI:5993805
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 54)
AUTHORS Schubert M., Harmison G G II, Chen, C.-J., and Banjerjee, A.
TITLE DNA constructs encoding CD4 fusion proteins
JOURNAL Patent: US 5847096-A 71 08-DEC-1998;
FEATURES Location/Qualifiers
1..54
source /organism="unknown"

BASE COUNT 14 a 18 c 10 g 12 t
ORIGIN

Query Match 0.8%; Score 23; DB 6; Length 54;
Best Local Similarity 74.4%; Pred. No. 8.4e+05;
Matches 29; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 910 AATATATATGTCGAAAAGAGACTGCTGCTGCTGGA 948
|||||
DB 40 AGTCGTCGAGGACGAAACAGCAGTGGGTCTGCTGATGA 2

RESULT 3
LOCUS A21609 37 bp DNA linear PAT 07-JUL-1994
DEFINITION oligonucleotide.
ACCESSION A21609
VERSION A21609 1 GI:583606
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
FEATURES Location/Qualifiers
1..37
source /organism="synthetic construct"

BASE COUNT 6 a 5 c 4 g 22 t
ORIGIN

Query Match 0.8%; Score 22.6; DB 6; Length 37;
Best Local Similarity 75.7%; Pred. No. 1e+06;
Matches 28; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2020 TGTATGAAAAAATGAATAGCTTTTATGAAAAAGA 2056
|||||
DB 37 TGTATGACAAAAAAGTCTCATGACAAAAA 1

RESULT 4
LOCUS AX381765 58 bp DNA linear PAT 18-MAR-2002

DEFINITION Sequence 703 from Patent WO0212280.
ACCESSION AX381765
VERSION AX381765.1 GI:19576587
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Fukariyota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Primates, Catarrhini, Hominoidea; Homo.

REFERENCE 1
AUTHORS Pyle, P. A., Xu, T. and Secrist, H.
TITLE Compositions and methods for the therapy and diagnosis of colon cancer
JOURNAL Patent: WO 0212280-A 703 14-FEB 2002;
CORIXA CORPORATION (US)
FEATURES Location/Qualifiers
1..58
source /organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 0 a 8 c 5 g 45 t
ORIGIN

Query Match 0.8%; Score 22.4; DB 6; Length 58;
Best Local Similarity 62.5%; Pred. No. 1.2e+06;
Matches 35; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 2110 GGAGAACACATTCATCAAGAAAGCATAAAGATCAAAATTAATAATTCGAGACC 2165
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DB 56 GGGAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGGGCC 1

RESULT 5
LOCUS AX011418 59 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 95 from Patent WO9555907.
ACCESSION AX011418
VERSION AX011418.1 GI:9997968
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 59)
AUTHORS Koetter, P., Entian, K. D. and Diu-Herard, A.
TITLE Method for screening antimycotic substances using essential genes from S. cerevisiae
JOURNAL Patent: WO 9555907-A 95 04-NOV-1999;
KOETTER PETER (DE); FNTIUS KAPL DIETEP (DE); DIU HERARD ANITA (FR); HOECHST MARION ROUSSEL INC (FR)
FEATURES Location/Qualifiers
1..59
source /organism="synthetic construct"
/db_xref="taxon:32630"
/note="primer YDR499w-S1"

BASE COUNT 16 a 11 c 18 g 14 t
ORIGIN

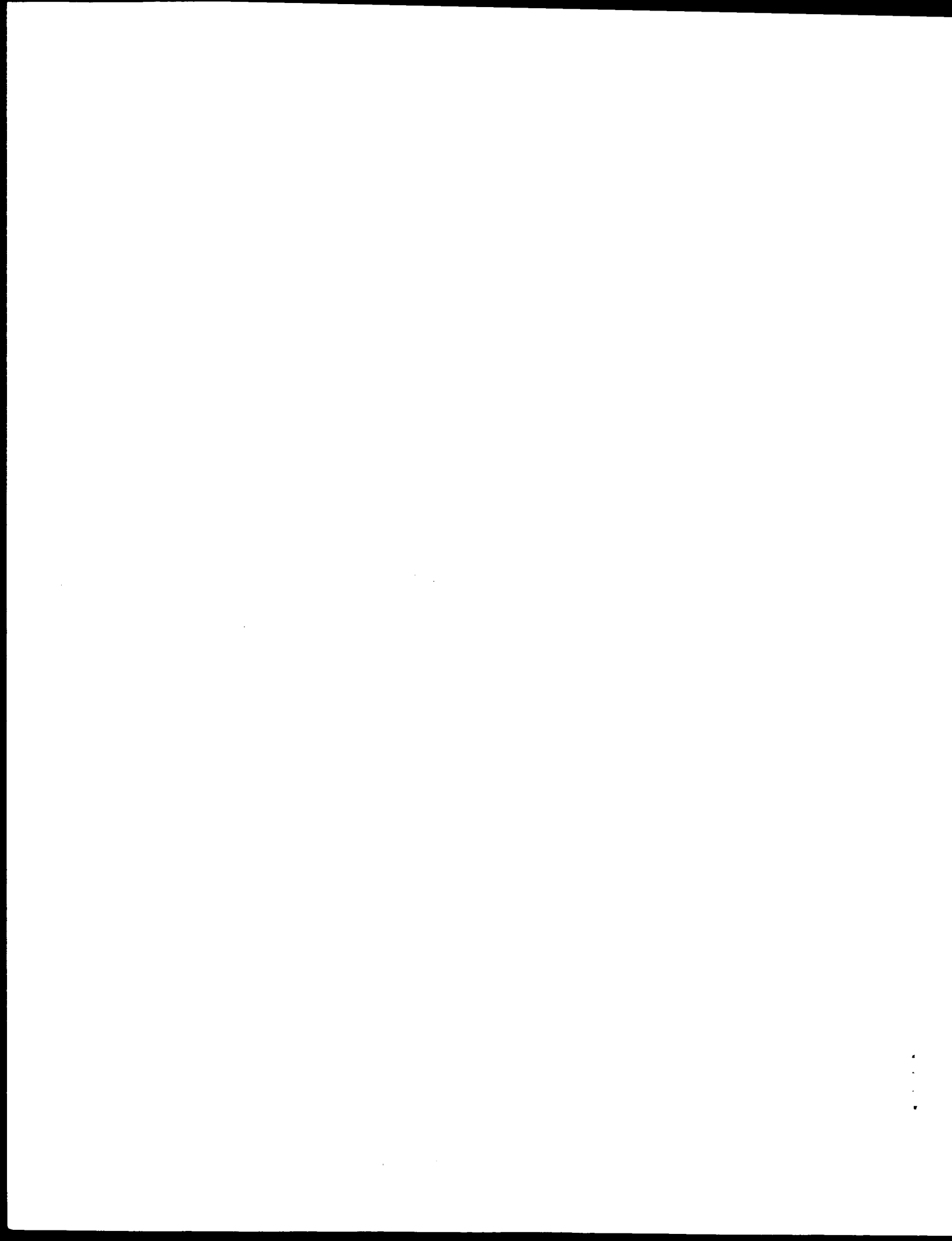
Query Match 0.8%; Score 22.4; DB 6; Length 59;
Best Local Similarity 72.5%; Pred. No. 1.2e+06;
Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1745 GAAGAGGCGCTCAACTTCTCCAGATGAGAACTAAAG 1784
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DB 10 GAAACGGTGGTCAATTTCTTCATGATGACGACCGGAAG 49

RESULT 6
LOCUS AR201911 60 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 14 from patent US 6361943.
ACCESSION AR201911
VERSION AR201911.1 GI:20256450
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

[illegible]

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Matches 28,		Conservative	0;	Mismatches 10;	
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Db	39	GTACTGTCATAGACCCCGAGGAGTGTGGACAGA	2		
RESULT 12					
AK151069/C					
LOCUS		AK151069			
DEFINITION		Sequence 9 from patent us 6231850.	39 bp	DNA	
ACCESSION		AK151069			
VERSION		AK151069.1	GI:1511719		
KEYWORDS		Unknown.			
SOURCE		Unknown.			
ORGANISM		Unknown.			
REFERENCE					
1.		(bases 1 to 39)			
AUTHORS		Okano,F., Satoh,M. and Yamada,K.			
TITLE		Canine interleukin 12			
JOURNAL		Patent: US 6231850-A	9	15-MAY-2001;	
FEATURES		Location/Qualifiers			
source		1..39			
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ORIGIN		/organism="unknown"			
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Matches 26,		Conservative	0;	Mismatches 7;	Ind
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Db	37	CAAGGAGGAGCTGGCGCTGCACATCTCCA	5		
RESULT 13					
LOCUS		E15025			
DEFINITION		PCR primer for canine interleukin 12	39 bp	DNA	line
ACCESSION		E15025			
VERSION		E15025.1	GI:5709708		
KEYWORDS		JP 1998036397-A/9.			
SOURCE		unidentified.			
ORGANISM		unidentified.			
REFERENCE		1.	(bases 1 to 39)		
AUTHORS		Okano,F.			
TITLE		CANINE INTERLEUKIN 12 AND ITS PRODUCTION			
JOURNAL		Patent: JP 1998036397-A	9	10-FEB-1998.	
COMMENT					
OS		None			
OC		Artificial sequences.			
PN		JP 1998036397-A/9			
PD		10-FEB-1998			
FF		08-NOV-1996	JP 1996296789		
PR		08-NOV-1995	JP 95P	289729,	23-MAY-1996
OKANO FUMIYOSHI					
PC		C07K14/34,C07H21/04	C12N5/10,C12N5/00,C12P2/		
		C12R1/91).			
CC		(C12P1/02,C12R1/91);			
CC		strandedness: Single;			
FH		topology: Linear;			
FH		Key			
FH		Location/Qualifiers			
FT		source	1..39		



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CM nucleic nucleic search, using SW model

Run on: Apr 16, 2003, 22:54:24 : Search time 389 Seconds
(without alignments)

10177.707 Million cell updates/sec

Title: US-09-954-679-3

Perfect score: 2928

Sequence: 1 aatcccaacttaccactcaaa.....gggcaactggatcatgaatt 2928

Scoring table:

IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Scored: 6,0749 seqs, 50220978 residues

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Minimum DB seq length: 0

Maximum DB seq length: 60

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications, NA.*

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- 2: /cqn2_6/prodata/1/pubpna/PCT_NEW_PUB.seq.*
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- 4: /cqn2_6/prodata/1/pubpna/US06_PUBCOMB.seq.*
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- 7: /cqn2_6/prodata/1/pubpna/US08_NEW_PUB.seq.*
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- 11: /cqn2_6/prodata/1/pubpna/US10_NEW_PUB.seq.*
- 12: /cqn2_6/prodata/1/pubpna/US10_PUBCOMB.seq.*
- 13: /cqn2_6/prodata/1/pubpna/US60_NEW_PUB.seq.*
- 14: /cqn2_6/prodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	22.4	0.8	58	10	US-09-919-580-703
2	22.4	0.8	63	9	US-10-228-070-14
3	22.4	0.8	63	12	US-10-046-722-14
4	22.2	0.8	51	9	US-09-764-872-151
5	21.8	0.7	60	7	US-08-781-986A-1652
6	21.6	0.7	60	9	US-09-362-286-22
7	21.4	0.7	60	10	US-09-919-580-419
8	21.2	0.7	52	7	US-08-781-986A-5071
9	20.8	0.7	59	10	US-09-855-159-2
10	20.8	0.7	59	12	US-10-013-737-12
11	20.6	0.7	57	7	US-08-781-986A-3384
12	20.4	0.7	57	9	US-10-199-330-12
13	20.4	0.7	57	9	US-10-199-334-12
14	20.2	0.7	47	9	US-09-758-017A-18
15	20.2	0.7	51	10	US-09-790-417-21
16	20	0.7	40	10	US-09-947-305-3
17	20	0.7	46	10	US-09-827-289-25
18	20	0.7	53	10	US-09-912-787-38
19	20	0.7	53	12	US-10-014-326-24

c	20	0.7	55	7	US-08-781-986A-2746	Sequence 2746, App
21	20	0.7	57	7	US-08-781-986A-4986	Sequence 4986, App
22	20	0.7	57	9	US-09-721-862-51	Sequence 51, Appl
23	20	0.7	57	9	US-10-083-557-444	Sequence 444, App
24	20	0.7	57	9	US-08-781-986A-3384	Sequence 3384, App
25	19.8	0.7	55	7	US-08-781-986A-3384	Sequence 3384, App
26	19.6	0.7	50	9	US-09-992-598-244	Sequence 244, App
27	19.6	0.7	50	9	US-09-989-754-244	Sequence 244, App
28	19.6	0.7	50	9	US-09-989-754-244	Sequence 244, App
29	19.6	0.7	50	9	US-09-990-444-244	Sequence 244, App
30	19.6	0.7	50	9	US-09-989-750-244	Sequence 244, App
31	19.6	0.7	50	9	US-09-990-446-244	Sequence 244, App
32	19.6	0.7	50	9	US-09-991-181-244	Sequence 244, App
33	19.6	0.7	50	9	US-09-994-687-244	Sequence 244, App
34	19.6	0.7	50	9	US-09-989-754-244	Sequence 244, App
35	19.6	0.7	50	9	US-09-997-654-244	Sequence 244, App
36	19.6	0.7	50	9	US-09-994-667-244	Sequence 244, App
37	19.6	0.7	50	9	US-09-990-448-244	Sequence 244, App
38	19.6	0.7	50	9	US-09-990-562-244	Sequence 244, App
39	19.6	0.7	50	9	US-09-997-428-244	Sequence 244, App
40	19.6	0.7	50	9	US-09-997-666-244	Sequence 244, App
41	19.6	0.7	50	9	US-09-990-711-244	Sequence 244, App
42	19.6	0.7	50	9	US-09-989-726-244	Sequence 244, App
43	19.6	0.7	50	9	US-09-990-447-244	Sequence 244, App
44	19.6	0.7	50	9	US-09-998-156-244	Sequence 244, App
45	19.6	0.7	50	9	US-09-991-157-244	Sequence 244, App

ALIGNMENTS

RESULT 1
US-09-919-580-703/c
: Sequence 703, Application US/09/919580
: Patent No. US20020110842A1
: GENERAL INFORMATION:
: APPLICANT: Pyrie, Ruth
: APPLICANT: Xu, Jianqun
: APPLICANT: Secrist, Heather
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
: FILE REFERENCE: 210121.552
: CURRENT APPLICATION NUMBER: US/09/919,580
: NUMBER OF SEQ ID NOS: 944
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 703
: LENGTH: 58
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-919-580-703

Query Match 0.8% Score 22.4; DB 10; Length 58;
Best Local Similarity 62.5%; Pred. No. 1,0004;
Matches 35; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
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DB 56 GGGGAAA 1

RESULT 2
US-10-228-070-14/c
: Sequence 14, Application US/10/228070
: Publication No. US20030322240A1
: GENERAL INFORMATION:
: APPLICANT: Hiroshi YANAGAWA et al.
: TITLE OF INVENTION: Molecule Assigning Genotype to
: Phenotype And Use Thereof
: NUMBER OF SEQUENCES: 26
: CORRESPONDENCE ADDRESS:
: ADDRESS: Wenderoth, Lind & Ponack, L.L.P.
: STREET: 2034 K Street, N.W., Suite 800

```
;
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/228,070
; FILING DATE: 27-Aug-2002
; CLASSIFICATION: (D) REFERENCE: 2002-1108/LC/01416
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 10/046,722
; FILING DATE: 17-Jan-02
; APPLICATION NUMBER: 09/284,627
; FILING DATE: 02-Jun-99
;
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 60
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: synthetic DNA
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; FEATURE:
; OTHER INFORMATION: has a sequence partly
; complementary to SEQ ID NO: 17
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-228-070-14

Query Match 0.8%; Score 22.4; DB 9; Length 60;
Best Local Similarity 66.7%; Pred. No. 1.2e+04;
Matches 32; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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; 55 GGGGAGGTCTATTAAAAAAGCAAGCAAGCAATATAAGATGCAATTAATAAATT 8
;
;
; RESULT 4
; US-09-764-872-151
; Sequence 151, Application US/09/764,872
; Publication No. US20030050231A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA125
; CURRENT APPLICATION NUMBER: US/09/764,872
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 957
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 151
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-764-872-151

Query Match 0.8%; Score 22.2; DB 9; Length 51;
Best Local Similarity 77.1%; Pred. No. 1.2e+04;
Matches 27; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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; 1750 GGTGGTTCACACCTTCCTCCAGATGAGCAAGCAAGCAAGCAAGCAAGCAAG 1784
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; RESULT 5
; US-08-781-986A-1652/c
; Sequence 1652, Application US/08/781,986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MS-DOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
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; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; FILING DATE: 27-Aug-2002
; CLASSIFICATION: (D) REFERENCE: 2002-1108/LC/01416
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 10/046,722
; FILING DATE: 17-Jan-02
; APPLICATION NUMBER: 09/284,627
; FILING DATE: 02-Jun-99
;
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 60
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: synthetic DNA
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; FEATURE:
; OTHER INFORMATION: has a sequence partly
; complementary to SEQ ID NO: 17
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-228-070-14

Query Match 0.8%; Score 22.4; DB 9; Length 60;
Best Local Similarity 66.7%; Pred. No. 1.2e+04;
Matches 32; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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; 55 GGGGAGGTCTATTAAAAAAGCAAGCAAGCAATATAAGATGCAATTAATAAATT 8
;
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; RESULT 3
; US-10-046-722-14/c
; Sequence 14, Application US/10/046,722
; Patent No. US20020072087A1
; GENERAL INFORMATION:
; APPLICANT: Hiroshi YANAGAWA et al.
; TITLE OF INVENTION: Molecule Assigning Genotype To Phenotype And Use Thereof
;
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wonderoth, Lind & Ponack, L.L.P.
; STREET: 2033 K Street, N.W., Suite 800
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/046,722
; FILING DATE: 17-Jan-2002
; CLASSIFICATION: (D) REFERENCE: 2001-1921/LC/01416
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/284,627
; FILING DATE: 02-Jun-99
;
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
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; Sequence 2, Application US/09855159
; Patent No. US20020042136A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020042136A1artis AG
; TITLE OF INVENTION: Retroviral vectors comprising an enhanced 3' transcription termin
; FILE REFERENCE: 4-31439A/USC
; CURRENT APPLICATION NUMBER: US/09/855,159
; CURRENT FILING DATE: 2001-05-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 59
; TYPE: DNA
; ORGANISM: Equine infectious anemia virus
US-09-855-159-2

Query Match          0.7%; Score 20.8; DB 10; Length 59;
Best Local Similarity 64.4%; Pred. No. 3.4e+04;
Matches 31; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 2106 ATTTGAGAAACAAATTGATGAGAAAGGATGAAAGATGAAATTA 2153
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RESULT 10
US-10-013-737-12/c
; Sequence 12, Application US/10013737
; Patent No. US20020115093A1
; GENERAL INFORMATION:
; APPLICANT: Reynolds, Mark A.
; APPLICANT: Ruvelo, Michael
; APPLICANT: Arnold, Jr., Lyle J.
; TITLE OF INVENTION: COMBINED POLYNUCLEOTIDE SEQUENCES AS DISCRETE ASSAY
; FILE REFERENCE: ENDOPOINTS
; CURRENT APPLICATION NUMBER: US/10/013,737
; CURRENT FILING DATE: 2001-11-12
; PRIOR APPLICATION NUMBER: US/04/5,42,456
; PRIOR FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: IPRI Program
; SEQ ID NO 12
; LENGTH: 59
; TYPE: DNA
; ORGANISM: Candida albicans
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020115093A1 P22S853
US-10-013-737-12

Query Match          0.7%; Score 20.8; DB 12; Length 59;
Best Local Similarity 70.0%; Pred. No. 3.4e+04;
Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1176 TTGCGAACTCAAGTCTTTTATTGATGAAATAATACAAAT 1215
      || ||||| ||| ||| || ||||| ||||| ||||| |||||
DB 43 TTGCGAAACGAAATATAAATATATGAAACATAAATAAT 4

RESULT 11
US-08-781-986A-3384/c
; Sequence 3384, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
```

```
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44M storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PR248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 3384:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 57 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-781-986A-3384

Query Match          0.7%; Score 20.6; DB 7; Length 57;
Best Local Similarity 67.4%; Pred. No. 3.9e+04;
Matches 29; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 648 AGTCTTTAAAGATTCTCTTTATGATGAGATGAGGAGATGATAA 590
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 44 AGGTATTAAGATTCTCTTCTTGAAGACATTGTGATCTTTCACCAACA 2

RESULT 12
US-10-199-330-12/c
; Sequence 12, Application US/10199330
; Publication No. US20020182681A1
; GENERAL INFORMATION:
; APPLICANT: WOODAGE, Trevor et al.
; TITLE OF INVENTION: ISOLATED HUMAN DRUG-METABOLIZING
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
; TITLE OF INVENTION: DRUG-METABOLIZING PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL000669DIV-1
; CURRENT APPLICATION NUMBER: US/10/199,330
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 09/609,816
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 60/192,408
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: 60/212,725
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: 09/609,816
; PRIOR FILING DATE: 2000-07-03
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 57
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-199-330-12

Query Match          0.7%; Score 20.4; DB 9; Length 57;
Best Local Similarity 65.2%; Pred. No. 4.4e+04;
Matches 30; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 2114 CAACACATTGATGAAGAAAGCATGAAATGAAATTAATAATG 2159
      ||| ||||| ||| ||||| ||||| ||||| ||||| ||||| |||
```

Db 57 GAATATTTGAAGAAAGACAGCAAAATGAGAGCACTTTAAAAATAG 12

RESULT 14

US 10 199 434 12/0

Sequence 12, Application US/1019434

Publication No. US2004008454A1

GENERAL INFORMATION:

APPLICANT: WOBIDGE, Trevor et al.

TITLE OF INVENTION: ISOLATED HUMAN DRUG-METABOLIZING

TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN

TITLE OF INVENTION: DRUG-METABOLIZING PROTEINS, AND USES THEREOF

FILE REFERENCE: CLO00669DIV-3

CURRENT APPLICATION NUMBER: US/10199434

PRIOR FILING DATE: 2002 07 22

PRIOR APPLICATION NUMBER: 09/609,816

PRIOR FILING DATE: 2001 04 27

PRIOR APPLICATION NUMBER: 60/192,408

PRIOR FILING DATE: 2000 03 27

PRIOR APPLICATION NUMBER: 60/212,725

PRIOR FILING DATE: 2000 06 20

PRIOR APPLICATION NUMBER: 09/609,816

PRIOR FILING DATE: 2000 07 03

NUMBER OF SEQ ID NOS: 23

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 12

LENGTH: 57

TYPE: DNA

ORGANISM: Homo sapiens

US 10 199 434 12

Query Match 0.7% Score 20.4; DB 9; Length 57;

Best Local Similarity 65.2% Pred. No. 4.4e+04;

Matches 30; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

OY 2114 GAACACATTGATGAAGCAAAAGCATAAAAGATGAAATTAATAATTTG 2159

Db 57 GAATATTTGAAGAAAGACAGCAAAATGAGAGCACTTTAAAAATAG 12

RESULT 14

US 09 758 017A 18

Sequence 18, Application US/09758017A

Patent No. US2002015557A1

GENERAL INFORMATION:

APPLICANT: Lanes, Olav

APPLICANT: Willasen, Nils Peder

APPLICANT: Guddal, Per Henrik

APPLICANT: Gjellesvik, Bør Rune

TITLE OF INVENTION: Codon-optimized DNA glycosylase, gene coding therefor,

TITLE OF INVENTION: recombinant DNA containing said gene or operative parts

TITLE OF INVENTION: thereof, a method for preparing said protein and the

TITLE OF INVENTION: thereof, a method for preparing said protein and the

FILE REFERENCE: U013209-4

CURRENT APPLICATION NUMBER: US/09758,017A

PRIOR FILING DATE: 2001 01 10

PRIOR APPLICATION NUMBER: 2000 5428

PRIOR FILING DATE: 2000 10 27

PRIOR APPLICATION NUMBER: 2000 0163

PRIOR FILING DATE: 2000 01 12

NUMBER OF SEQ ID NOS: 19

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO 18

LENGTH: 47

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Artificial

OTHER INFORMATION: Sequence - Primer used to prepare rcuNG gene

US 09 758 017A 18

Query Match 0.7% Score 20.2; DB 9; Length 47;

Best Local Similarity 68.4% Pred. No. 4.4e+04;

Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

OY 593 CTCGAGCAAAACAGCGGACAGGCTCTCATGCAATGCTGCTCA 633

Db 4 CTCGAGCAAAACAGAGGCTGAGGCTCTCTCATGCAATGCTGCTCA 44

RESULT 15

US-09-790-417-241

Sequence 241, Application US/09790417

Patent No. US20010031470A1

GENERAL INFORMATION:

APPLICANT: Shultz, John W

APPLICANT: Lewis, Martin K.

APPLICANT: Lieppe, Donna

APPLICANT: Mandrekar, Michelle

APPLICANT: Kephart, Daniel

APPLICANT: Rhodes, Richard R.

APPLICANT: Andrews, Christine A.

APPLICANT: Hartnett, James R.

APPLICANT: Gu, Trent

APPLICANT: Olson, Ryan J.

APPLICANT: Wood, Keith W.

APPLICANT: Welch, Roy

TITLE OF INVENTION: Nucleic Acid Detection

FILE REFERENCE: Pro-103 6868/75528

CURRENT APPLICATION NUMBER: US/09790,417

CURRENT FILING DATE: 2001 02 22

PRIOR APPLICATION NUMBER: 09/458,972

PRIOR FILING DATE: 1999 07 21

PRIOR APPLICATION NUMBER: 09/042,287

PRIOR FILING DATE: 1998 03 13

NUMBER OF SEQ ID NOS: 290

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO 23

LENGTH: 51

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: primer for EST

OTHER INFORMATION: restriction site

US-09-790-417-241

Query Match 0.7% Score 20.2; DB 10; Length 51;

Best Local Similarity 68.4% Pred. No. 4.7e+04;

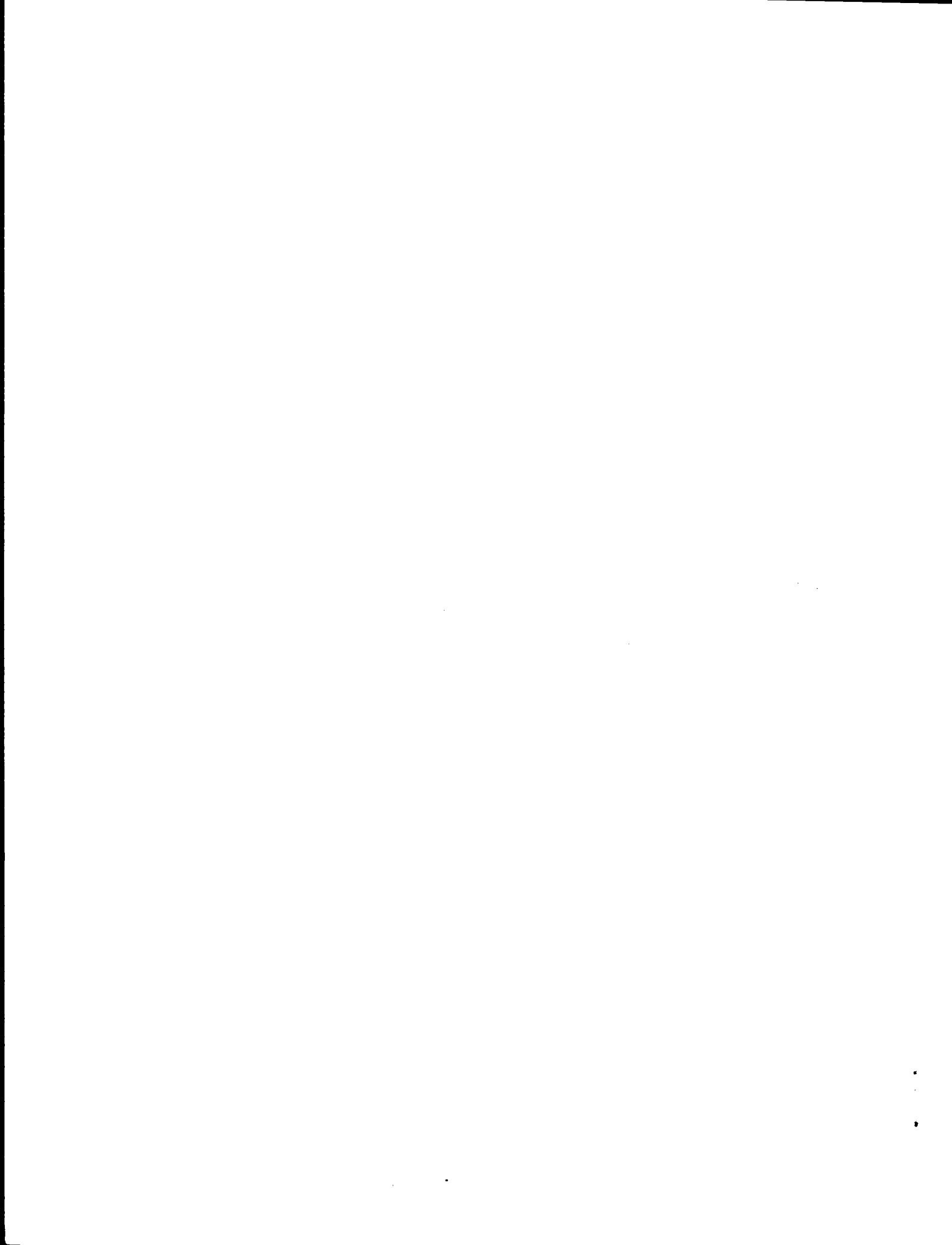
Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

OY 769 GCATGCTGCTGTCGACATGCGGCTGATGTCACATGTCAGG 809

Db 1 GCTTAAGCTGACAGGCGCATGCTGTCGATGATGTCGTCGTCG 41

Search completed: April 17, 2003, 04:35:29

Job time : 307 secs



Genre version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

Model selection using SW model

Run on: April 16, 2003, 22:41:29 ; Search time 4479 Seconds
(without alignments)
10587.271 Million cell updates/sec

```

Title: US-09-954 679-3
Perfect score: 2928
Sequence: 1 aaTCCCAATTACACTCAGG.....GAGCACTCCATCATCAATT 2928

```

Scoring table: IDENTITY_NOK
gapexp 10.0 , gapext 1.0

```

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 146654

```

Minimum DB seq length: 0
Maximum DB seq length: 60

Post processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

```

EST; *
Database;
1: cm est ba; *
2: cm est hum; *

```

3: `em_estim:` ★
4: `em_estim:` ★
5: `em_estcv:` ★

```
6: cm_estpl: ★
7: cm_estro: ★
8: cm_hlc: ★
```

```

9; qb_est 1; *
10; qb_est 2; *
11; qb_hfc; *

```

12: qb, est 3; *
13: qb, est 4; *
14: qb, est 5; *
15: qb, est 6; *

15: em. est. l. un.; ★
16: em. est. l. om.; ★
17: qb. qss.; ★
18: em. est. l. om.; ★

18: `qm_qss_hum; *`
19: `qm_qss_inv; *`
20: `qm_qss_pln; *`
21: `qm_qss_vrt; *`

21: `em_qss_vr1`; \star
 22: `em_qss_1m`; \star
 23: `em_qss_mam`; \star
 24: `em_qss_mis`; \star

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24: em_qss_mads: *
25: em_qss_other: *
26: em_qss_pro: *
27: em_qss_red: *

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prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.

SUMMARIES

Result	Score	Query Match	Length	DH	ID	Description
1	100	100	100	100	100	100
2	95	95	95	95	95	95
3	90	90	90	90	90	90
4	85	85	85	85	85	85
5	80	80	80	80	80	80
6	75	75	75	75	75	75
7	70	70	70	70	70	70
8	65	65	65	65	65	65
9	60	60	60	60	60	60
10	55	55	55	55	55	55
11	50	50	50	50	50	50
12	45	45	45	45	45	45
13	40	40	40	40	40	40
14	35	35	35	35	35	35
15	30	30	30	30	30	30
16	25	25	25	25	25	25
17	20	20	20	20	20	20
18	15	15	15	15	15	15
19	10	10	10	10	10	10
20	5	5	5	5	5	5

Run	Time (h)	Temp (°C)	Pressure (atm)	Yield (%)	Product
1	27.8	0.9	58	14	H05434
2	27.4	0.9	58	17	H05434
					BH623868
					BH623868
					10070

3	26.6	0.9	60	14	R85541	R85541	yo38c01
4	26	0.9	52	9	AA782923	AA782923	ai62c01
5	25.6	0.9	59	14	N24179	N24179	yx69c08

ϵ	b	$2^{5,2}$	0.9	55	13	HG943565	aX391
						HG943565	aX391

Query Match	0.9%	Score 25.2	DB 13	Length 55	LOCUS	A523624	60 bp	mRNA	linear	EST 13-APR-1999
Best Local Similarity	66.7%	pred No. 1.2e-05			DEFINITION	t959b12.x1	NCI_CGAP_CLL1	Homo sapiens	cDNA clone IMAGE:211511	
Matches 36	Conservative	0	Mismatches 18	Indels 0	Gaps 0			similar to	qb:X57025_rnal	INSULIN-LIKE GROWTH FACTOR I A PRECURSOR


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/clone="IMAGE:4950911"
/clone_lib="NCI_CGAP_Mam6"
/sex="female_virgin"
/lissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10H"
/notes="Organ. Mammary. Vector. pCMV SpORF6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"

BASE COUNT      37 a      1 c      9 g      13 t
ORIGIN

Query Match      0.8%; Score 24; DB 13; Length 60;
Best Local Similarity 64.1%; Pred. No. 2 6e+05;
Matches 36; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 2105 AATTTCGACAGACATTTTTCAGCAAGAAACGATATAAAAGATGAAATTAATAATTC 2160
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 4 AATTTCAGAGTAATAATTTTTCAGCAAGAAACGATATAAAAGAAAGAAAAAAGG 59

RESULT 11
LOCUS      HG671284
DEFINITION      54 bp mRNA linear EST 30-APR-2001
ACCESSION      BG671284
VERSION        BG671284.1 GI:13893383
KEYWORDS       EST.
SOURCE         Norway rat.
ORGANISM       Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE      1 (bases 1 to 54)
AUTHORS        Xiao, H.S., Huang, Q.H., Zhang, F.X., Rao, L., Lu, Y.J., Guo, C., Yang, L.,
Huang, W.J., Fu, G., Xu, S.H., Cheng, X.P., Yan, Q., Zhu, Z.D., Zhang
X., Chen, Z., Han, Z.G. and Zhang, X.
TITLE          Identification of gene expression profile of dorsal root ganglion
JOURNAL        Proc. Natl. Acad. Sci. U.S.A. 99 (12), 8360-8366 (2002)
MEDLINE        22056133
COMMENT        Contact: Zhang Xu
Laboratory of Sensory System
Institute of Neuroscience
320 Yue Yang Road, Shanghai 200031, P R China
Tel: 86-21-64748700-121
Fax: 86-21-64713446
Email: xu.zhang@ion.ac.cn
This clone is also available at Chinese National Human Genome
Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park,
Pudong New Area, P.R.China. Please contact with Zhang Xu
(xu.zhang@ion.ac.cn) or Han Zeguang (hanzg@chgc.sh.cn)
PCR Primers
FORWARD: T3
BACKWARD: T7
Seq primer: T3
POLYA-No.

Location/Qualifiers
1..54
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="DRNR0A12"
/clone_lib="Rat DRG Library"
/sex="male"
/tissue_type="dorsal root ganglion"
/dev_stage="adult"
/notes="Total RNA was isolated from hypothalamus and
transcribed into cDNA, which was then used as template in
PCR. The PCR products were separated on sequencing gel.
The differential bands were cut, reamplified, cloned into

/clone="IMAGE:5125241"
/clone_lib="NCI_CGAP_Li9"
/lab_host="DH10H (TI phage-resistant)"
/notes="Organ. Liver; Vector: pCMV-SpORF6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT      17 a      15 c      17 g      10 t
ORIGIN

Query Match      0.8%; Score 23.8; DB 13; Length 59;
Best Local Similarity 72.1%; Pred. No. 2 9e+05;
Matches 31; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 2687 TGAGGAACCTTCAGACTCAGACAGCTGTGAGTCTACTTGGCCCAACA 2729
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 3 TGAGGAACCTTCAGACTCAGACAGAGGCTTCACATTTGTTCAAGA 45

RESULT 13
LOCUS      B1148041
DEFINITION      602912577F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:505355 5'
ACCESSION      B1148041
VERSION        B1148041.1 GI:14508042
KEYWORDS       EST.
SOURCE         house mouse.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 59)
AUTHORS        NIH-MGC http://mgi.nci.nih.gov/
TITLE          National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL        Unpublished (1999)
COMMENT        Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Jeffrey R. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/HLN at:
http://image.llnl.gov
Plate: LLAM1306 row: e column: 18
High quality sequence stop: 59.
Location/Qualifiers
1..59
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5125241"
/clone_lib="NCI_CGAP_Li9"
/lab_host="DH10H (TI phage-resistant)"
/notes="Organ. Liver; Vector: pCMV-SpORF6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT      33 a      2 c      6 g      13 t
ORIGIN

Query Match      0.8%; Score 23.8; DB 12; Length 54;
Best Local Similarity 80.0%; Pred. No. 2.8e+05;
Matches 28; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2006 AGATTATGAATGTGTATGAAAAAATGAATA 2040
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 14 AAGTATATGAATGTGTATGAAAAAATGAATA 48

RESULT 12
LOCUS      B1246744
DEFINITION      602959667F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:5125241 5'
ACCESSION      B1246744
VERSION        B1246744.1 GI:14791003
KEYWORDS       EST.
SOURCE         house mouse.
ORGANISM       Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 59)
AUTHORS        NIH-MGC http://mgi.nci.nih.gov/
TITLE          National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL        Unpublished (1999)
COMMENT        Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Jeffrey R. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/HLN at:
http://image.llnl.gov
Plate: LLAM1306 row: e column: 18
High quality sequence stop: 59.
Location/Qualifiers
1..59
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5125241"
/clone_lib="NCI_CGAP_Li9"
/lab_host="DH10H (TI phage-resistant)"
/notes="Organ. Liver; Vector: pCMV-SpORF6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT      17 a      15 c      17 g      10 t
ORIGIN

Query Match      0.8%; Score 23.8; DB 13; Length 59;
Best Local Similarity 72.1%; Pred. No. 2 9e+05;
Matches 31; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 2687 TGAGGAACCTTCAGACTCAGACAGCTGTGAGTCTACTTGGCCCAACA 2729
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 3 TGAGGAACCTTCAGACTCAGACAGAGGCTTCACATTTGTTCAAGA 45

RESULT 13
LOCUS      B1148041
DEFINITION      602912577F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:505355 5'
ACCESSION      B1148041
VERSION        B1148041.1 GI:14508042
KEYWORDS       EST.
SOURCE         house mouse.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 59)
AUTHORS        NIH-MGC http://mgi.nci.nih.gov/
TITLE          National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL        Unpublished (1999)
COMMENT        Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Jeffrey R. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/HLN at:
http://image.llnl.gov
Plate: LLAM1306 row: e column: 18
High quality sequence stop: 59.
Location/Qualifiers
1..59
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5125241"
/clone_lib="NCI_CGAP_Li9"
/lab_host="DH10H (TI phage-resistant)"
/notes="Organ. Liver; Vector: pCMV-SpORF6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT      33 a      2 c      6 g      13 t
ORIGIN

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Matches 31; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Oy 2864 TCTCATTCATTTCAGTTCAGTATTATTGAGCATCTAGTATAAGTC 2907

Db 3 TTTTTCATTCAACAAGCTCTTTATTGAGGACCTTACTCTCTGCC 46

Search completed: April 17, 2003, 02:29:52
Job time : 4485 secs

Genome version 5.1.3
Copyright (c) 1993 2003 CompuGen Ltd.

us-09-954-679-3

Run on: April 16, 2003, 22:43:09 ; Search time 111 Seconds
(without alignments)
8089.636 Million cell updates/sec

Title: us-09-954-679-3

Perfect score: 2928

Sequence: 1 aatcccaattacactcaaa.....gggaactggatgatgaatt 2928

Scoring table: IDENTITY_NOC

Gapop 10.0 , Gapext 1.0

Sequences: 441362 seqs, 1533838 residues

Total number of hits satisfying chosen parameters: 645134

Minimum DB seq length: 0

Maximum DB seq length: 60

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : ISSUED PATENTS NA:*

- 1: /cqn2_6/ptodata/1/ina/5A_COMB.seq.*
- 2: /cqn2_6/ptodata/1/ina/5B_COMB.seq.*
- 3: /cqn2_6/ptodata/1/ina/6A_COMB.seq.*
- 4: /cqn2_6/ptodata/1/ina/6B_COMB.seq.*
- 5: /cqn2_6/ptodata/1/ina/pcTUS_COMB.seq.*
- 6: /cqn2_6/ptodata/1/ina/backtiltest.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49.4	1.7	51	4	US-08-973-005A-4
2	35	1.2	35	4	US-08-973-005A-7
3	35	1.2	35	4	US-08-973-005A-8
4	25	0.9	48	1	US-08-783-275-6
5	25	0.9	48	1	US-08-727-708-6
6	23	0.8	54	2	US-08-418-848A-71
7	22.6	0.8	47	1	US-07-867-106-6
8	22.4	0.8	60	4	US-09-284-627-14
9	22.2	0.8	60	4	US-09-344-888A-7
10	21.8	0.7	39	4	US-09-079-984A-9
11	21.6	0.7	47	4	US-09-641-638-770
12	21.6	0.7	51	1	US-08-379-926A-2
13	21.6	0.7	51	1	US-08-379-926A-3
14	21	0.7	60	2	US-08-454-257-9
15	21	0.7	60	2	US-09-062-375-9
16	21	0.7	60	3	US-09-203-796A-9
17	20.8	0.7	59	4	US-09-542-656-12
18	20.8	0.7	60	4	US-09-188-086-12
19	20.6	0.7	45	1	US-08-483-415-21
20	20.6	0.7	45	6	5487983-18
21	20.6	0.7	54	4	US-09-171-162B-7
22	20.6	0.7	54	4	US-09-171-162B-8
23	20.4	0.7	57	4	US-09-609-816-12
24	20.2	0.7	46	4	US-09-406-074-1
25	20.2	0.7	47	4	US-09-641-638-758
26	20.2	0.7	51	4	US-09-358-972-231
27	20.2	0.7	51	4	US-09-430-615-21

28	20.2	0.7	58	4	US-08-860-038-16
29	20.2	0.7	58	4	US-09-580-923-16
30	20.2	0.7	60	2	US-08-117-952-760
31	20	0.7	40	2	US-08-942-521B-4
32	20	0.7	40	4	US-09-192-792-4
33	20	0.7	40	4	US-08-445-474-4
34	20	0.7	40	5	PCT US94 02612-4
35	20	0.7	46	1	US-07-915-245-4
36	20	0.7	47	4	US-09-641-638-774
37	20	0.7	53	1	US-08-258-025A-16
38	20	0.7	53	5	PCT US95 07541-16
39	19.8	0.7	27	4	US-08-584-040-1424
40	19.8	0.7	35	2	US-08-583-276-9
41	19.8	0.7	45	2	US-08-583-276-10
42	19.8	0.7	47	4	US-09-641-638-1219
43	19.8	0.7	48	2	US-08-883-795A-13
44	19.8	0.7	50	2	US-08-053-451B-106
45	19.8	0.7	57	2	US-08-117-981-1

ALIGNMENTS

RESULT 1

US-08-973-005A-4

Sequence 4, Application US/08974005A

Patent No. 6320099

GENERAL INFORMATION:

APPLICANT: OGAWA, Toshiya

YOSHIOKA Masaharu

ISHIDA Tsao

TITLE OF INVENTION: VIRUS RESISTANT PLANTS EXPRESSING ANIMAL

CELL DERIVED (2' 5') OLIGONUCLEOTIDE SYNTHETASE AND

RIBONUCLEASE L AND A METHOD FOR CREATING THE SAME

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Polcy & Lardner

STREET: 4000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC DOS/MS DOS

SOFTWARE: Patent In Release #1.0, Version #1.00

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08973,005A

FILING DATE: 01 Dec 1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 134741/1995

FILING DATE: 31-MAY 1995

APPLICATION NUMBER: JP 285401/1995

FILING DATE: 01-NOV 1995

APPLICATION NUMBER: JP 52010/1996

FILING DATE: 08 MAR 1996

ATTORNEY/AGENT INFORMATION:

NAME: Bent, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 081456/0113

TELEPHONE: (202)672-5400

TELEFAX: (202)672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 51 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc - "Synthetic DNA"

CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobel, Martens, Olson & Bear
STREET: 620 Newport Center Drive, 16th Floor
CITY: Newport Beach
STATE: CA

COUNTRY: U.S.A.

ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ Version 1.5

APPLICATION NUMBER: US/08/727,708

FILING DATE: 15 JAN 1997

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/727,708

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Bartfield, Neil S

REGISTRATION NUMBER: 49,901

REFERENCE/DOCKET NUMBER: 1MSC1.001A

TELEPHONE: 619 245-8550

TELEFAX: 619 245-0176

TELEX:

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 48 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US 08 783 275 6

Query Match 0.9%; Score 25; DB 1; Length 48;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 648 GGACACGTACAGGCTTGAGGATTC 662

db 1 GGACACGTACAGGCTTGAGGATTC 25

RESULT 5

US 08 727 708 6

Sequence 6; Application US/08/727708

Patent No. 5,776,690

GENERAL INFORMATION:

APPLICANT: Voljant, Aristo

APPLICANT: Mordechai, Eli

TITLE OF INVENTION: RIBONUCLEASE L INHIBITOR AS

TITLE OF INVENTION: AN INDICATOR OF CHRONIC FATIGUE SYNDROM

TITLE OF INVENTION: E

TITLE OF INVENTION: E

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Knobel, Martens, Olson & Bear

STREET: 620 Newport Center Drive, 16th Floor

CITY: Newport Beach

STATE: CA

COUNTRY: U.S.A.

ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/727,708

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bartfield, Neil S
REGISTRATION NUMBER: 49,901
REFERENCE/DOCKET NUMBER: 1MSC1.001A
TELEPHONE: 619 245-8550
TELEFAX: 619 245-0176
TELEX:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US 08 727 708 6

Query Match 0.9%; Score 25; DB 1; Length 48;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 638 GGACACGTACAGGCTTGAGGATTC 662

db 1 GGACACGTACAGGCTTGAGGATTC 25

RESULT 6

US 08 418-848A 71/C

Sequence 71; Application US/08418848A

Patent No. 5847096

GENERAL INFORMATION:

APPLICANT: SCHUBERT, MANFRED, HARMISON II,

APPLICANT: GEORGE G., CHANG JIE, CHEN, HANJIE/EA, AKHIL

TITLE OF INVENTION: DEFECTIVE, INTERFERING

TITLE OF INVENTION: HIV PARTICLES

NUMBER OF SEQUENCES: 77

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN, L.L.P.

STREET: 445 PARK AVENUE

CITY: NEW YORK

COUNTRY: U.S.A.

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC DOS/MS DOS

SOFTWARE: WORD PERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/418,848A

FILING DATE: 07 APR 1995

CLASSIFICATION: 526

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/946,849

FILING DATE: 28 AUG 1992

CLASSIFICATION: 526

ATTORNEY/AGENT INFORMATION:

NAME: RICHARD W. BORK

REGISTRATION NUMBER: 46,459

REFERENCE/DOCKET NUMBER: 2026 4091052

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-758 4800

TELEFAX: 212-751 6849

TELEX: 421792

INFORMATION FOR SEQ ID NO: 71:

SEQUENCE CHARACTERISTICS:

LENGTH: 54 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-418-848A-71

Query Match 0.8%; Score 24; DB 2; Length 54;
Best Local Similarity 74.4%; Pred. No. 1.5e+03;

Query Match 0 7%; Score 21.6; DB 1; length 51;
Best Local Similarity 68.2%; Pred. No. 3.8e+03;
Matches 30; Conservative 0; Mismatches 14; Indels

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; STATE: CA
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE
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